

<400> 2

097637105300

Met Pro Thr Ser Gly Thr Thr Ile Glu Leu Ile Asp Asp Gln Phe Pro  
1 5 10 15  
Lys Asp Asp Ser Ala Ser Ser Gly Ile Val Asp Glu Val Asp Leu Thr  
20 25 30  
Glu Ala Asn Ile Leu Ala Thr Gly Leu Asn Lys Lys Ala Pro Arg Ile  
35 40 45  
Val Asn Gly Phe Gly Ser Leu Met Gly Ser Lys Glu Met Val Ser Val  
50 55 60  
Glu Phe Asp Lys Lys Gly Asn Glu Lys Lys Ser Asn Leu Asp Arg Leu  
65 70 75 80  
Leu Glu Lys Asp Asn Gln Glu Lys Glu Glu Ala Lys Thr Lys Ile His  
85 90 95  
Ile Ser Glu Gln Pro Trp Thr Leu Asn Asn Trp His Gln His Leu Asn  
100 105 110  
Trp Leu Asn Met Val Leu Val Cys Gly Met Pro Met Ile Gly Trp Tyr  
115 120 125  
Phe Ala Leu Ser Gly Lys Val Pro Leu His Leu Asn Val Phe Leu Phe  
130 135 140  
Ser Val Phe Tyr Tyr Ala Val Gly Gly Val Ser Ile Thr Ala Gly Tyr  
145 150 155 160  
His Arg Leu Trp Ser His Arg Ser Tyr Ser Ala His Trp Pro Leu Arg  
165 170 175  
Leu Phe Tyr Ala Ile Phe Gly Cys Ala Ser Val Glu Gly Ser Ala Lys  
180 185 190  
Trp Trp Gly His Ser His Arg Ile His His Arg Tyr Thr Asp Thr Leu  
195 200 205  
Arg Asp Pro Tyr Asp Ala Arg Arg Gly Leu Trp Tyr Ser His Met Gly  
210 215 220  
Trp Met Leu Leu Lys Pro Asn Pro Lys Tyr Lys Ala Arg Ala Asp Ile  
225 230 235 240  
Thr Asp Met Thr Asp Asp Trp Thr Ile Arg Phe Gln His Arg His Tyr  
245 250 255  
Ile Leu Leu Met Leu Leu Thr Ala Phe Val Ile Pro Thr Leu Ile Cys  
260 265 270  
Gly Tyr Phe Phe Asn Asp Tyr Met Gly Gly Leu Ile Tyr Ala Gly Phe  
275 280 285  
Ile Arg Val Phe Val Ile Gln Ala Thr Phe Cys Ile Asn Ser Leu  
290 295 300  
Ala His Tyr Ile Gly Thr Gln Pro Phe Asp Asp Arg Arg Thr Pro Arg  
305 310 315 320  
Asp Asn Trp Ile Thr Ala Ile Val Thr Phe Gly Glu Gly Tyr His Asn  
325 330 335  
Phe His His Glu Phe Pro Thr Asp Tyr Arg Asn Ala Ile Lys Trp Tyr  
340 345 350  
Gln Tyr Asp Pro Thr Lys Val Ile Ile Tyr Leu Thr Ser Leu Val Gly  
355 360 365  
Leu Ala Tyr Asp Leu Lys Lys Phe Ser Gln Asn Ala Ile Glu Glu Ala  
370 375 380  
Leu Ile Gln Gln Glu Gln Lys Lys Ile Asn Lys Lys Lys Ala Lys Ile  
385 390 395 400  
Asn Trp Gly Pro Val Leu Thr Asp Leu Pro Met Trp Asp Lys Gln Thr  
405 410 415  
Phe Leu Ala Lys Ser Lys Glu Asn Lys Gly Leu Val Ile Ile Ser Gly  
420 425 430  
Ile Val His Asp Val Ser Gly Tyr Ile Ser Glu His Pro Gly Gly Glu  
435 440 445  
Thr Leu Ile Lys Thr Ala Leu Gly Lys Asp Ala Thr Lys Ala Phe Ser  
450 455 460  
Gly Gly Val Tyr Arg His Ser Asn Ala Ala Gln Asn Val Leu Ala Asp

09763331.053004

3

465                      470                      475                      480  
 Met Arg Val Ala Val Ile Lys Glu Ser Lys Asn Ser Ala Ile Arg Met  
                                  485                      490                      495  
 Ala Ser Lys Arg Gly Glu Ile Tyr Glu Thr Gly Lys Phe Phe  
                                  500                      505                      510

&lt;210&gt; 3

&lt;211&gt; 1555

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthetic yeast delta-9 desaturase gene modified  
 for expression in plants

&lt;400&gt; 3

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ggatccaaca atgctactt ctggaactac tatcgagctt atcgatgatc aattccctaa      60
ggatgattct gcttcttctg gaatcgttga tgaggttgat cttactgagg ctaacatcct    120
tgctactgga cttacaaga aggctcctag aatcgttaac ggattcggat ctcttatggg    180
atctaaggag atggtttctg ttgagttcga taagaaggga aacgagaaga agtctaacct    240
tgatagactt cttgagaagg ataaccaaga gaaggaggag gctaagacta agatccatat    300
ctctgagcaa ccttggaact tcaacaactg gcatcaacat ctcaactggc tcaacatggg    360
gctcgtctgt ggaatgccta tgatcggatg gtacttcgct ctctctggaa aagtgcctct    420
ccatctcaac gttttcctct tctctgtctt ctactacgct gttggaggag tgtctatcac    480
tgctggatac catagactct ggtctcatag atcttactct gctcattggc ctcttagact    540
cttctacgct atctttggat gtgcttctgt tgagggatct gctaagtggg ggggacattc    600
tcatagaatc catcatagat aactgatac tcttagagat ccttacgatg ctagaagagg    660
actttggtac tctcatatgg gatggatgct tcttaagcct aaccctaagt acaaggctag    720
agctgatatc actgatatga ctgatgattg gactatcaga tccaacata gacattacat    780
cttgctctag ctcttactg ctttcgtgat cctactctc atctgtggat acttcttcaa    840
cgattacatg ggaggactca tctacgctgg attcatcaga gtgttcgtca tccaacaagc    900
tactttctgt atcaactcta tggctcatta catcggaact caacctttcg atgatagaag    960
aactcctaga gataactgga tcaactgctat cgttactttc ggagagggat accataactt   1020
ccatcatgag ttccctactg attatagaaa cgctatcaag tggtaaccaat acgatcctac   1080
taaagtgatc atctacttga cttctctcgt gggacttgct tacgatctca agaagttctc   1140
tcaaaacgct atcgaggagg ctcttatcca acaagagcaa aagaagatca acaagaagaa   1200
ggctaagatt aattggggac ctgttcttac tgatcttctt atgtgggata agcaaaacttt   1260
ccttgctaag tctaaggaga acaagggact tgttatcatc tctggaatcg ttcgatgatg   1320
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gcttgctgat atgagagttg ctgttatcaa ggagtctaag aactctgcta tcagaatggc   1500
ttctaagaga ggagagatct acgagactgg aaagttcttc tgatctagag gatcc       1555

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&lt;210&gt; 4

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 4

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Met Gly Ala Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
 1           5           10          15
Glu Thr Asp Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
          20          25          30
Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
          35          40          45
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
          50          55          60
Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65           70           75           80

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0963371.053001

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
                             85                            90                            95  
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
                             100                            105                            110  
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser  
                             115                            120                            125  
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His  
                             130                            135                            140  
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
                             145                            150                            155                            160  
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu  
                             165                            170                            175  
 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu  
                             180                            185                            190  
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys  
                             195                            200                            205  
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln  
                             210                            215                            220  
 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr  
                             225                            230                            235                            240  
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly  
                             245                            250                            255  
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu  
                             260                            265                            270  
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp  
                             275                            280                            285  
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu  
                             290                            295                            300  
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu  
                             305                            310                            315                            320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile  
                             325                            330                            335  
 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr  
                             340                            345                            350  
 Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp  
                             355                            360                            365  
 Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu  
                             370                            375                            380

&lt;210&gt; 5

&lt;211&gt; 1372

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 5

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ctacttcttc	caagaaatcg	gaaaccgaca	ccacaaagcg	tgtgccgtgc	gagaaaccgc	180
ctttctcggt	gggagatctg	aagaaagcaa	tcccgccgca	ttgtttcaaa	cgctcaatcc	240
ctcgctcttt	ctcctacctt	atcagtgaca	tcattatagc	ctcatgcttc	tactacgtcg	300
ccaccaatta	cttctctctc	ctccctcagc	ctctctctta	cttggttgg	ccactctatt	360
gggcctgtca	aggctgtgtc	ctaactggta	tctgggtcat	agcccacgaa	tgcggtcacc	420
acgcattcag	cgactaccaa	tggttggtg	acacagttgg	tcttatcttc	cattccttcc	480
tcctcgctcc	ttactttctc	tggaagtata	gtcatcgccg	tcaccattcc	aacactggat	540
ccctcgaaag	agatgaagta	tttgtcccaa	agcagaaatc	agcaatcaag	tggtacggga	600
aatacctcaa	caaccctctt	ggacgcacat	tgatgttaac	cgtccagttt	gtcctcgggt	660
ggccttgta	cttagccttt	aacgtctctg	gcagaccgta	tgacgggttc	gcttgccatt	720
tcttcccaa	cgctcccatc	tacaatgacc	gagaacgcct	ccagatatac	ctctctgatg	780
cgggtattct	agccgtctgt	tttggctctt	accgttacgc	tgctgcacaa	gggatggcct	840

T00E50"TEEE9260

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tcaggggagc tttggctacc gtagacagag actacggaat cttgaacaag gtgttccaca     1020
acattacaga cacacacgtg gctcatcacc tgttctcgac aatgccgcat tataacgcaa     1080
tggaagctac aaaggcgata aagccaattc tgggagacta ttaccagttc gatggaacac     1140
cgtggtatgt agcgatgtat agggaggcaa aggagtgtat ctatgtagaa ccggacaggg     1200
aaggtgacaa gaaaggtgtg tactggtaca acaataagtt atgagcatga tggggaagaa     1260
attgtcgacc tttctcttgt ctgtttgtct tttgttaaag aagctatgct tcgttttaat     1320
aatcttattg tccattttgt tgtgttatga cattttggct gctcattatg tt              1372

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&lt;210&gt; 6

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 7

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Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu
 1              5              10              15
Pro Asp Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys
      20              25              30
Leu

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&lt;210&gt; 7

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces cerevisiae

&lt;400&gt; 7

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Met Arg Val Ala Val Ile Lys Glu Ser Lys Asn Ser Ala Ile Arg Met
 1              5              10              15
Ala Ser Lys Arg Gly Glu Ile Tyr Glu Thr Gly Lys Phe Phe
      20              25              30

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T00050" TEE29/60